

SEQUENCE LISTING

<110> Burnham, Martin K. R.

<120> dexB

<130> GM10087

<150> 60/057,876

<151> 1997-09-02

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<212> DNA

<213> Streptococcus pneumoniae

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<221> CDS

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aag agt ttt atg gat agt aat gga gat gga gtt ggt gat ttg cca ggt  
96

Lys Ser Phe Met Asp Ser Asn Gly Asp Gly Val Gly Asp Leu Pro Gly  
20 25 30

att acc agt aag ttg gac tat cta gct aag tta gga atc aca tcg att  
144

Ile Thr Ser Lys Leu Asp Tyr Leu Ala Lys Leu Gly Ile Thr Ser Ile

35

40

45

tgg ctt tct ccc gtt tat gac agc cct atg gat gat aat ggc tac gat  
192

Trp Leu Ser Pro Val Tyr Asp Ser Pro Met Asp Asp Asn Gly Tyr Asp  
50 55 60

att gct gat tat caa gcg att gcg gct att ttt gga acc atg gag gac  
240

Ile Ala Asp Tyr Gln Ala Ile Ala Ala Ile Phe Gly Thr Met Glu Asp  
65 70 75 80

atg gat gaa ctg att gca gaa gct aag aag cgt gat atc cgt atc atc  
288

Met Asp Glu Leu Ile Ala Glu Ala Lys Lys Arg Asp Ile Arg Ile Ile  
85 90 95

atg gac ttg gtg gtc aat cat acc tcg gat gag cat gcc tgg ttt gta  
336

Met Asp Leu Val Val Asn His Thr Ser Asp Glu His Ala Trp Phe Val  
100 105 110

gag gcc tgt gaa aat cct aat agc cct gag cga gac tac tat atc tgg  
384

Glu Ala Cys Glu Asn Pro Asn Ser Pro Glu Arg Asp Tyr Tyr Ile Trp  
115 120 125

cgc gat gaa ccc aat gac cta gat tct atc ttt agt ggg tct gct tgg  
432

Arg Asp Glu Pro Asn Asp Leu Asp Ser Ile Phe Ser Gly Ser Ala Trp  
130 135 140

gaa tac gat gaa aag tca ggt caa tac tat ctc cac ttt ttc agc aag  
480

Glu Tyr Asp Glu Lys Ser Gly Gln Tyr Tyr Leu His Phe Phe Ser Lys  
145 150 155 160

aaa cag ccg gat ctc aac tgg gaa aat gaa aaa ctt cgc cag aaa att  
528

Lys Gln Pro Asp Leu Asn Trp Glu Asn Glu Lys Leu Arg Gln Lys Ile

165

170

175

576 tat gag atg atg aac ttc tgg att gat aag ggt att ggt ggt ttc cgt

Tyr Glu Met Met Asn Phe Trp Ile Asp Lys Gly Ile Gly Gly Phe Arg

180

185

190

624 atg gat gtt att gac atg att ggc aaa att cct gac gag aag gta gtc

Met Asp Val Ile Asp Met Ile Gly Lys Ile Pro Asp Glu Lys Val Val

195

200

205

672 aat aat ggt cct atg ctc cat ccc tat ctc aag gaa atg aat cag gcg

Asn Asn Gly Pro Met Leu His Pro Tyr Leu Lys Glu Met Asn Gln Ala

210

215

220

720 acc ttt gga gat aag gat ctc ttg aca gta ggg gag act tgg gga gca

Thr Phe Gly Asp Lys Asp Leu Leu Thr Val Gly Glu Thr Trp Gly Ala

225

230

235

240

768 acg cca gag att gcc aaa ctc tac tct gat cca aag ggg caa gaa ttg

Thr Pro Glu Ile Ala Lys Leu Tyr Ser Asp Pro Lys Gly Gln Glu Leu

245

250

255

816 tct atg gtc ttc cag ttt gaa cat atc ggt ctt cag tat cag gaa ggt

Ser Met Val Phe Gln Phe Glu His Ile Gly Leu Gln Tyr Gln Glu Gly

260

265

270

864 cag cct aaa tgg cac tat caa aaa gag ctg aat atc gct aag tta aaa

Gln Pro Lys Trp His Tyr Gln Lys Glu Leu Asn Ile Ala Lys Leu Lys

275

280

285

912 gaa atc ttc aac aaa tgg cag aca gag tta gga gtt gag gac ggc tgg

Glu Ile Phe Asn Lys Trp Gln Thr Glu Leu Gly Val Glu Asp Gly Trp

290

295

300

aat tcc ctc ttc tgg aac aac cat gac ctc cct cgt att gtc tca atc  
960

Asn Ser Leu Phe Trp Asn Asn His Asp Leu Pro Arg Ile Val Ser Ile  
305 310 315 320

tgg gga aat gac caa gaa tac cgc gaa aaa tct gcc aaa gcc ttt gca  
1008

Trp Gly Asn Asp Gln Glu Tyr Arg Glu Lys Ser Ala Lys Ala Phe Ala  
325 330 335

atc ttg ctt cat ctt atg aga gga act cct tat atc tac caa ggt gag  
1056

Ile Leu Leu His Leu Met Arg Gly Thr Pro Tyr Ile Tyr Gln Gly Glu  
340 345 350

gag att ggg atg acc aac tat ccg ttt gaa aca ctg gat caa gta gaa  
1104

Glu Ile Gly Met Thr Asn Tyr Pro Phe Glu Thr Leu Asp Gln Val Glu  
355 360 365

gat att gaa tct ctc aac tat gcg cgt gag gct ctt gaa aaa ggt gtt  
1152

Asp Ile Glu Ser Leu Asn Tyr Ala Arg Glu Ala Leu Glu Lys Gly Val  
370 375 380

ccg atg caa gaa atc atg gac agt atc cgt gtt att gga cgt gac aat  
1200

Pro Met Gln Glu Ile Met Asp Ser Ile Arg Val Ile Gly Arg Asp Asn  
385 390 395 400

gcc cgt acc cct atg caa tgg gac gag agc aaa aac gct ggt ttc tca  
1248

Ala Arg Thr Pro Met Gln Trp Asp Glu Ser Lys Asn Ala Gly Phe Ser  
405 410 415

aca ggt caa cct tgg ttg gca gtt aat cca aat tac gag atg atc aac  
1296

Thr Gly Gln Pro Trp Leu Ala Val Asn Pro Asn Tyr Glu Met Ile Asn

420                    425                    430

gtc caa gaa gcg ctg gca aat cca gat tct att ttc tat acc tat cag  
1344  
Val Gln Glu Ala Leu Ala Asn Pro Asp Ser Ile Phe Tyr Thr Tyr Gln  
435                    440                    445

aaa ctg gtc caa att cgc aag gag aat agt tgg cta att cga gct gac  
1392  
Lys Leu Val Gln Ile Arg Lys Glu Asn Ser Trp Leu Ile Arg Ala Asp  
450                    455                    460

ttt gaa ttg ctt gat acg gct gat aag gtc ttt gct tat ata cgt aag  
1440  
Phe Glu Leu Leu Asp Thr Ala Asp Lys Val Phe Ala Tyr Ile Arg Lys  
465                    470                    475                    480

gat ggc gac cgt cgc ttc cta gtt gtg gct aac ttg tcc aat gaa gag  
1488  
Asp Gly Asp Arg Arg Phe Leu Val Val Ala Asn Leu Ser Asn Glu Glu  
485                    490                    495

caa gac ttg aca gta gaa gga aaa gtc aaa tct gtc ttg att gaa aac  
1536  
Gln Asp Leu Thr Val Glu Gly Lys Val Lys Ser Val Leu Ile Glu Asn  
500                    505                    510

acc cta gct caa gaa gtc ttt gaa aaa caa atc tta gtt cca tgg gat  
1584  
Thr Leu Ala Gln Glu Val Phe Glu Lys Gln Ile Leu Val Pro Trp Asp  
515                    520                    525

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1608  
Ala Phe Cys Val Glu Leu Leu  
530                    535

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<213> Streptococcus pneumoniae

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			20						25				30		
Ile	Thr	Ser	Lys	Leu	Asp	Tyr	Leu	Ala	Lys	Leu	Gly	Ile	Thr	Ser	Ile
			35					40				45			
Trp	Leu	Ser	Pro	Val	Tyr	Asp	Ser	Pro	Met	Asp	Asp	Asn	Gly	Tyr	Asp
	50				55					60					
Ile	Ala	Asp	Tyr	Gln	Ala	Ile	Ala	Ala	Ile	Phe	Gly	Thr	Met	Glu	Asp
65					70					75			80		
Met	Asp	Glu	Leu	Ile	Ala	Glu	Ala	Lys	Lys	Arg	Asp	Ile	Arg	Ile	Ile
			85					90				95			
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		100				105					110				
Glu	Ala	Cys	Glu	Asn	Pro	Asn	Ser	Pro	Glu	Arg	Asp	Tyr	Tyr	Ile	Trp
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Arg	Asp	Glu	Pro	Asn	Asp	Leu	Asp	Ser	Ile	Phe	Ser	Gly	Ser	Ala	Trp
		130			135					140					
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145				150					155			160			
Lys	Gln	Pro	Asp	Leu	Asn	Trp	Glu	Asn	Glu	Lys	Leu	Arg	Gln	Lys	Ile
			165			170				175					
Tyr	Glu	Met	Met	Asn	Phe	Trp	Ile	Asp	Lys	Gly	Ile	Gly	Gly	Phe	Arg
			180			185				190					
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			195			200				205					
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			210			215				220					
Thr	Phe	Gly	Asp	Lys	Asp	Leu	Leu	Thr	Val	Gly	Glu	Thr	Trp	Gly	Ala
225				230					235			240			
Thr	Pro	Glu	Ile	Ala	Lys	Leu	Tyr	Ser	Asp	Pro	Lys	Gly	Gln	Glu	Leu
			245			250				255					
Ser	Met	Val	Phe	Gln	Phe	Glu	His	Ile	Gly	Leu	Gln	Tyr	Gln	Glu	Gly
			260			265				270					
Gln	Pro	Lys	Trp	His	Tyr	Gln	Lys	Glu	Leu	Asn	Ile	Ala	Lys	Leu	Lys
			275			280				285					

Glu Ile Phe Asn Lys Trp Gln Thr Glu Leu Gly Val Glu Asp Gly Trp  
290 295 300  
Asn Ser Leu Phe Trp Asn Asn His Asp Leu Pro Arg Ile Val Ser Ile  
305 310 315 320  
Trp Gly Asn Asp Gln Glu Tyr Arg Glu Lys Ser Ala Lys Ala Phe Ala  
325 330 335  
Ile Leu Leu His Leu Met Arg Gly Thr Pro Tyr Ile Tyr Gln Gly Glu  
340 345 350  
Glu Ile Gly Met Thr Asn Tyr Pro Phe Glu Thr Leu Asp Gln Val Glu  
355 360 365  
Asp Ile Glu Ser Leu Asn Tyr Ala Arg Glu Ala Leu Glu Lys Gly Val  
370 375 380  
Pro Met Gln Glu Ile Met Asp Ser Ile Arg Val Ile Gly Arg Asp Asn  
385 390 395 400  
Ala Arg Thr Pro Met Gln Trp Asp Glu Ser Lys Asn Ala Gly Phe Ser  
405 410 415  
Thr Gly Gln Pro Trp Leu Ala Val Asn Pro Asn Tyr Glu Met Ile Asn  
420 425 430  
Val Gln Glu Ala Leu Ala Asn Pro Asp Ser Ile Phe Tyr Thr Tyr Gln  
435 440 445  
Lys Leu Val Gln Ile Arg Lys Glu Asn Ser Trp Leu Ile Arg Ala Asp  
450 455 460  
Phe Glu Leu Leu Asp Thr Ala Asp Lys Val Phe Ala Tyr Ile Arg Lys  
465 470 475 480  
Asp Gly Asp Arg Arg Phe Leu Val Val Ala Asn Leu Ser Asn Glu Glu  
485 490 495  
Gln Asp Leu Thr Val Glu Gly Lys Val Lys Ser Val Leu Ile Glu Asn  
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